What is claimed is:

1. A genetically modified coryneform bacterium, wherein its fadD15 gene, which codes for acyl-CoA synthase, is amplified.

2. The genetically modified coryneform bacterium as claimed in claim 1, wherein the starting bacterium (wild-type) is selected from the group consisting of Corynebacterium glutamicum (ATCC13032), Corynebacterium acetoglutamicum (ATCC15806), Corynebacterium acetoacidophilum (ATCC13870), Corynebacterium thermoaminogenes (FERM BP-1539), Corynebacterium melassecola (ATCC17965), Brevibacterium flavum (ATCC14067), Brevibacterium lactofermentum (ATCC13869) and Brevibacterium divaricatum (ATCC14020), or is selected from the group consisting of Corynebacterium glutamicum FERM-P 1709, Brevibacterium flavum FERM-P 1708, Brevibacterium lactofermentum FERM-P 1712, Corynebacterium glutamicum FERM-P 6463, Corynebacterium glutamicum FERM-P 6464 and Corynebacterium glutamicum DSM5715.

3. The genetically modified coryneform bacterium as claimed in claim 1, wherein the amplification of the fadD15 gene is carried out by over-expression of the gene.

4. The genetically modified coyneform bacterium as claimed in claim 3, wherein amplification is by increasing the number of copies of the gene, by choosing a potent promoter or a regulation region above the reading frame, by mutation of the promoter, by mutation of the regulation region, by mutation of the ribosome binding site, by incorporation of a suitable expression cassette above the structural gene, by incorporation of inducible promoters, by prolonging the life of the corresponding mRNA, by a

reduced degradation of the proteins expressed, or by combination of several of these possibilities.

5. The genetically modified coryneform bacterium as claimed in claim 1, wherein the strain is transformed with a plasmid vector and the plasmid vector carries the nucleotide sequence which codes for the fadD15 gene.

6. The genetically modified coryneform bacterium as claimed in claim 1, which corresponds genotypically to the strain *Corynebacterium glutamicum* DSM 13249.

7. An isolated polynucleotide from coryneform bacteria, comprising a polynucleotide sequence selected from the group consisting of

   a) a polynucleotide which is homologous to the extent of at least 70% to a polynucleotide which codes for a polypeptide which comprises the amino acid sequence of SEQ ID No. 2, or consists of this,

   b) a polynucleotide which codes for a polypeptide which comprises an amino acid sequence which is homologous to the extent of at least 70% to the amino acid sequence of SEQ ID No. 2,

   c) a polynucleotide which is complementary to the polynucleotides of a) or b), and

   d) a polynucleotide comprising at least 15 successive nucleotides of the polynucleotide sequence of a), b) or c).

8. The polynucleotide as claimed in claim 7,wherein the polynucleotide is a recombinant DNA which is capable of replication in coryneform bacteria.

9. The polynucleotide as claimed in claim 7,wherein the polynucleotide is an RNA.

10. The polynucleotide as claimed in claim 8, wherein the DNA which is capable of replication, and comprises

(i) the nucleotide sequence shown in SEQ ID No. 1, or

(ii) at least one sequence which corresponds to sequence (i) in the context of the degeneration of the genetic code, or

(iii) at least one sequence which hybridizes with the sequence complementary to sequence(i) or (ii).

11. The polynucleotide as claimed in claim 10, wherein the DNA further comprises

(iv) mutations of neutral function in (i) which lead to homologous amino acids.

12. The polynucleotide sequence as claimed in claim 8, 9 or 10, which codes for a polypeptide which has the amino acid sequence SEQ ID No. 2.

13. A method for the fermentative preparation of L-amino acids, which comprises carrying out the following step:

a) fermenting coryneform bacteria which produce L-amino acids and in which at least the fadD15 gene or nucleotide sequences which code for it is amplified, in particular over-expressed.

14. The method according to claim 13 further comprising:

b) concentrating the L-amino acid in the medium or in the cells of the bacteria.

15. The method according to claim 14 further comprising:

c) isolating the L-amino acid.

16. The method as claimed in claim 13, wherein a genetically modified coryneform bacterium, wherein its fadD15 gene, which codes for acyl-CoA synthase, is amplified is employed.

17. The method as claimed in claim 13, wherein further genes which code a protein of the biosynthesis pathway of the desired L-amino acid are additionally amplified in the bacteria.

18. The method as claimed in claim 13, wherein metabolic pathways which reduce the formation of the desired amino acid are at least partly eliminated in the bacteria.

19. The method as claimed in claim 13, wherein the amino acid prepared is L-lysine.

20. The method as claimed in claim 13, wherein for the preparation of lysine, bacteria in which at the same time one or more genes selected from the group consisting of

a) the dapA gene which codes for dihydrodipicolinate synthase,

b) the dapE gene which codes for succinyl diaminopimelate desuccinylase,

c) the lysC gene which codes for a feed-back resistant aspartate kinase,

d) the tpi gene which codes for triose phosphate isomerase,

e) the gap gene which codes for glyceraldehyde 3-phosphate dehydrogenase,

f) the pgk gene which codes for 3-phosphoglycerate kinase,

g) the pyc gene which codes for pyruvate carboxylase,

h) the mqo gene which codes for malate:quinone oxidoreductase, and

i) the lysE gene which codes for lysine export,

is or are amplified, in particular over-expressed or amplified at the same time are fermented.

21. The method as claimed in claim 20, wherein said one or more genes is or are overexpressed at the same time are fermented.

22. A method as claimed in claim 13, wherein for the preparation of L-lysine, bacteria in which one or more genes selected from the group consisting of

a) the pck gene which codes for phosphoenol pyruvate carboxykinase,

b) the pgi gene which codes for glucose 6-phosphate isomerase, and

c) the poxB gene which codes for pyruvate oxidase,

is or are attenuated at the same time are fermented.

23. A primer which comprises a polynucleotide sequences or parts thereof as claimed in claim 7 and can produce DNA of genes which code for acyl-CoA synthase by the polymer chain reaction.

24. A hybridization probe which comprises a polynucleotide sequences as claimed in claim 7 and can isolate cDNA or genes which have a high homology with the sequence of the fadD15 gene.